



Blast 2 Sequences results

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Taxonomy

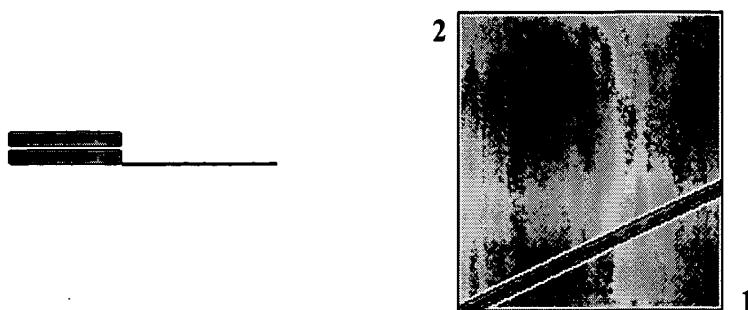
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Matrix **BLOSUM62** ▼ gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0** wordsize: **3** Filter Align

Sequence 1 lcl|seq_1 Length 167 (1 .. 167)

Sequence 2 lcl|seq_2 Length 397 (1 .. 397)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 339 bits (870), Expect = 1e-92
Identities = 167/167 (100%), Positives = 167/167 (100%)

Query: 1 MHWGTLCGFLWLWPYLFYVQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTLGL 60
MHWGTLCGFLWLWPYLFYVQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTLGL
Sbjct: 1 MHWGTLCGFLWLWPYLFYVQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTLGL 60

Query: 61 DFIPGLHPILTLSKMDQTLAVYQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLP 120
DFIPGLHPILTLSKMDQTLAVYQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLP
Sbjct: 61 DFIPGLHPILTLSKMDQTLAVYQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLP 120

Query: 121 WASGLETLDSLGGVLEASGYSTEVVVALSRLQGSLQDMLWQLDLSPGC 167
WASGLETLDSLGGVLEASGYSTEVVVALSRLQGSLQDMLWQLDLSPGC
Sbjct: 121 WASGLETLDSLGGVLEASGYSTEVVVALSRLQGSLQDMLWQLDLSPGC 167

CPU time: 0.02 user secs. 0.00 sys. secs 0.02 total secs.

Lambda	K	H
0.321	0.136	0.415

Gapped		
Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 586
Number of Sequences: 0
Number of extensions: 38

Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 167
length of database: 476,809,632
effective HSP length: 117
effective length of query: 50
effective length of database: 476,809,515
effective search space: 23840475750
effective search space used: 23840475750
T: 9
A: 40
X1: 16 (7.4 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.9 bits)
S2: 69 (31.2 bits)